

XX W6102: (left entry)
AC
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XX 01-0CF-1898
XX
XX Rat *ESK2* protein.
XX
XX Rat conductance calcium-activated potassium ion flux.
XX
XX Small conductance calcium ion flux.
XX
XX *ESK2*: rat potassium ion
XX

[illegible]

DK DNA encoding calcium-activated
XX To identify compounds where
PT the proteins of the invention,
PT Co identified potassium channel
XX Claim 2: page 94-95: 15pp; English.
XX The rat small conductance calcium-activated
PS ion channel (SK2) is the rat small conductance calcium-activated
PS between 40 and 60 pS when the channel is activated by between 2 and 60 pM and is

XX This sequence is a piece of a carboxyl molecule of between potassium protein.
CC potassium are monomers calculated form of a potassium protein.
CC inventomer: (1) has a unit conductance specific for the presence of the
CC inventomer: (1) has a unit conductance specific for the presence of the

CC the monomer and (ii) functionalized to well-defined linear
CC 80 kDa; and in the functionalized monomer, host compounds which trans-
CC monomer is in a xerophyll compound. Host compounds which trans-
CC specific for the DNA can be used to identify the protein of the p-
CC increased the area in a well-defined protein of the p-

CC express specific sequences through productions in 3;
CC probes or DNA sequence assays for flux mutations by the s
CC protein can be used in the recombinant mutations by the s
CC protein can be used for determining their Gops
CC protein can be used for determining their Gops

CC decrease also be used for determining ligands?
CC cell can also be used for determining ligands?
CC DNA sequences can also be used for determining
CC ligands in a computer system for determining
CC ligands in a computer system for determining

- - - 56

CC genes to be used in
CC structure, which is used
CC structure, which is used
CC proteins.

[illegible]

Queue Match	Similarity	3	Match
Best Local	570	Conservative	91.00
Queue Match	Similarity	3	Match
Best Local	570	Conservative	91.00

[illegible]

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116 NIGYKUSHRAT-
THAREIOLENDROM

119K191-211
137 119K191-211
Db 176 137111

100

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Page 2

XX M0601139-AL.
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XX 19-MAR-1998.
XX
XX 10-SEP-1997: 97NO-0516033.
XX
XX 17-APR-1997: 97NO-044233.
XX
XX 11-SEP-1996: 9605-0024451.
XX
XX 07-MAR-1997: 9705-0040052.
XX
XX (ICGC-) ONCOMI INC.
XX (ONCOMI-) ONCOMI HEALTH SCI.
XX
XX Adelman JP, Bond CT, Maylie J, Silvia CP:
XX
XX WPI: 1998-20732/18.
XX
XX N-PSDB: V35472.
XX
XX DNA encoding calcium-activated potassium channel - useful in assays
XX to identify compounds which increase or decrease potassium ion flux
XX
XX Claim 2: Page 126-128: 151pp: English.
XX
XX This sequence is the human small conductance calcium-activated
XX potassium channel protein 3 (hSK3) of the invention. The proteins of the
XX invention are monomers of a calcium-activated potassium channel, where
XX the monomer is a polypeptide chain of between 40 and 60 kDa and the
XX monomer is (1) has a unit conductance of between 2 and 60 pS when the
XX monomer is in the functional polymeric form of a potassium chain and is
XX specific for the potassium ion, and (2) is a polypeptide chain of between
XX 40 and 60 kDa. The protein can be used to detect the presence of the
XX protein or DNA sequences in a sample. Host cells expression of the
XX protein can be used in assays to identify compounds which increase or
XX decrease potassium ion flux through the protein. The transfected host
XX cells can also be used for determining mutations in the SK and IK
XX genes in a computer system for determining their three dimensional
XX structure, which is useful for determining ligands that bind to the
XX protein.
XX
XX Sequence 736 AA:
XX
XX Query Match 72.0% Score 2125.5; DB 19; Length 736;
XX Best Local Similarity 73.2%; Pred. No. 14-192; Index 37; Gaps 4;
XX Matches 428; Conservative 46; Mismatches 72; Indels 7; Gaps 4;
XX
XX 1 MSECNCNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 60
XX 180 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 218
XX
XX 61 SNAELVSEENRNNNSALATGTCG-----QSTGCGCGCGSNGSSCTGASRYN 114
XX 219 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 268
XX 115 ONTCVGLORARALRYKRYKLYALATFQRYVYVYTFRTSGKAWKASGLAKCL 174
XX 269 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 318
XX 329 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 368
XX 375 SASTLGLTGLVWARGIQPDWQADQDQDQDQDQDQDQDQDQDQDQDQDQDQ 414
XX 429 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 474
XX 435 PTFNALKASASTSTVDVDTDLSTFPEKFLALANRWLCHXKTKTSGNSGLAMK 294
XX 489 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 534
XX 535 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 574
XX 589 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 624
XX 639 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 674
XX 689 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 714
XX 736 MSECNCGMPSFSAHNRKNCNPGKQAPFASVCGCGASPSMAAANAAS 736

XX 355 TSTSTGCGMPCVTCGCGCTGTCMGCCTATVAVVAKETATKRNHPMOTO 414
XX 505 TLEISGWDHPSYKSGVCLTLLVHAGSCALVYVAFALAKKSHKFMNDQ 468
XX 415 LTRFNAANVLEKMTLYKMTLYKMTLYKMTLYKMTLYKMTLYKMTLYKMT 474
XX 569 LKTLKASANVLEKMTLYKMTLYKMTLYKMTLYKMTLYKMTLYKMTLYKMT 428
XX 475 QANTVLAKTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQ 534
XX 529 QNTVLAKTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQ 588
XX 535 QNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQ 574
XX 689 QNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQNTQ 733
XX
XX RESULT 5
XX M63715
XX ID M63715 standard: Protein: 732 AA.
XX AC M63715:
XX
XX 01-OCT-1998 (first entry)
XX
XX DE Rat fSK3 protein.
XX
XX Small conductance calcium-activated potassium channel protein 3:
XX fSK3; rat; potassium ion flux.
XX
XX Rattus sp.
XX
XX M0601139-AL.
XX
XX 10-SEP-1997: 97NO-0516033.
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XX 17-APR-1997: 9705-004233.
XX
XX 11-SEP-1996: 9605-0024451.
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XX 07-MAR-1997: 9705-0040052.
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XX genes in a computer system for determining their three dimensional
XX structure, which is useful for determining ligands that bind to the
XX protein.
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[illegible][illegible]

	cdt 131
	rda 283
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	tta 177
	yts 343
	atg 235
	kae 403
	koe 295
	acr 463
	natf 352
	sma 523
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	kida 405

molecular

Protein	Accession	Score	Length	Ident	Positives	Score	Length	Ident	Positives
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Protein 4	Q9JL46	463	352	1	1	463	352	1	1
Protein 5	Q9JL46	463	352	1	1	463	352	1	1
Protein 6	Q9JL46	463	352	1	1	463	352	1	1
Protein 7	Q9JL46	463	352	1	1	463	352	1	1
Protein 8	Q9JL46	463	352	1	1	463	352	1	1
Protein 9	Q9JL46	463	352	1	1	463	352	1	1
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Protein 11	Q9JL46	463	352	1	1	463	352	1	1
Protein 12	Q9JL46	463	352	1	1	463	352	1	1
Protein 13	Q9JL46	463	352	1	1	463	352	1	1
Protein 14	Q9JL46	463	352	1	1	463	352	1	1
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Protein 16	Q9JL46	463	352	1	1	463	352	1	1
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Protein 43	Q9JL46	463	352	1	1				

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Page 2

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GDMPGEN version 4.5
Copyright (c) 1995 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using pw model

Run on: May 14, 2001, 23:02:34 ; Search time 2221.07 seconds

11543.170 Million cell updates/sec

Title: US-09-254-590-21

Sequence: 11740

1 ATGGAGCGTCAGCTGACGTCMA.....CTTCATGACGAGTACTGAC 1740

Scoring table: IDENTITY, NUC
Gapop 10.0 / Gapext 1.0

Searched: 1283235 seqs, 737329552 residues

Total number of hits satisfying chosen parameters: 256470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Genbank
1: gb_bat1.*
2: gb_bat2.*
3: gb_bat3.*
4: gb_bat4.*
5: gb_bat5.*
6: gb_bat6.*
7: gb_bat7.*
8: gb_bat8.*
9: gb_bat9.*
10: gb_bat10.*
11: gb_bat11.*
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93: gb_bat93.*
94: gb_bat94.*
95: gb_bat95.*

Print. No. 14. The number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1732	99.5	2510 88	AF236613
2	1732	99.5	2510 88	AF236613
3	1240.6	71.3	2237 8	AF079312
4	803.8	46.2	2224 55	AF079312
5	802.2	46.1	2553 94	AF232189
6	780	44.8	2521 88	AF031815
7	778.8	44.6	2595 93	AF031815
8	778.8	44.6	2595 93	AF031815
9	651.4	37.2	1611 94	AF000973
10	647.6	37.2	1377 95	AF000973

[illegible][illegible]

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Page 18

Job time: 8325 sec

* * *

OM of: US-09-254-590-19 to: EST: * out_format : pfs
Date: May 14, 2001 9:00 PM
software version 4.5

[illegible]

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Database: uc01
Database sequences: 9623517
Database length: 73081774
Search time (sec): 1120.600000
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[illegible][illegible]

Blat20, v1.0.0. Arrayed by: Greg Lennon, Ph.D.
cDNA library Arrayed by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage.llnl.gov
Seq primer: 1400P from Glenco
Seq primer: 1400P from Glenco
High quality sequence stop: 482.
High quality clones/qualifiers

BASE COUNT

157 a	174 b	175 c	176 d	177 e	178 f	179 g	180 h	181 i	182 j	183 k	184 l	185 m	186 n	187 o	188 p	189 q	190 r	191 s	192 t	193 u	194 v	195 w	196 x	197 y	198 z	199 aa	200 ab	201 ac	202 ad	203 ae	204 af	205 ag	206 ah	207 ai	208 aj	209 ak	210 al	211 am	212 an	213 ao	214 ap	215 aq	216 ar	217 as	218 at	219 au	220 av	221 aw	222 ax	223 ay	224 az	225 ba	226 bb	227 bc	228 bd	229 be	230 bf	231 bg	232 bh	233 bi	234 bj	235 bk	236 bl	237 bm	238 bn	239 bo	240 bp	241 bq	242 br	243 bs	244 bt	245 bu	246 bv	247 bw	248 bx	249 by	250 bz	251 ca	252 cb	253 cc	254 cd	255 ce	256 cf	257 cg	258 ch	259 ci	260 cj	261 ck	262 cl	263 cm	264 cn	265 co	266 cp	267 cq	268 cr	269 cs	270 ct	271 cu	272 cv	273 cw	274 cx	275 cy	276 cz	277 da	278 db	279 dc	280 dd	281 de	282 df	283 dg	284 dh	285 di	286 dj	287 dk	288 dl	289 dm	290 dn	291 do	292 dp	293 dq	294 dr	295 ds	296 dt	297 du	298 dv	299 dw	300 dx	301 dy	302 dz	303 ea	304 eb	305 ec	306 ed	307 ee	308 ef	309 eg	310 eh	311 ei	312 ej	313 ek	314 el	315 em	316 en	317 eo	318 ep	319 eq	320 er	321 es	322 et	323 eu	324 ev	325 ew	326 ex	327 ey	328 ez	329 fa	330 fb	331 fc	332 fd	333 fe	334 ff	335 fg	336 fh	337 fi	338 fj	339 fk	340 fl	341 fm	342 fn	343 fo	344 fp	345 fq	346 fr	347 fs	348 ft	349 fu	350 fv	351 fw	352 fx	353 fy	354 fz	355 ga	356 gb	357 gc	358 gd	359 ge	360 gf	361 gg	362 gh	363 gi	364 gj	365 gk	366 gl	367 gm	368 gn	369 go	370 gp	371 gq	372 gr	373 gs	374 gt	375 gu	376 gv	377 gw	378 gx	379 gy	380 gz	381 ha	382 hb	383 hc	384 hd	385 he	386 hf	387 hg	388 hh	389 hi	390 hj	391 hk	392 hl	393 hm	394 hn	395 ho	396 hp	397 hq	398 hr	399 hs	400 ht	401 hu	402 hv	403 hw	404 hx	405 hy	406 hz	407 ia	408 ib	409 ic	410 id	411 ie	412 if	413 ig	414 ih	415 ii	416 ij	417 ik	418 il	419 im	420 in	421 io	422 ip	423 iq	424 ir	425 is	426 it	427 iu	428 iv	429 iw	430 ix	431 iy	432 iz	433 ja	434 jb	435 jc	436 jd	437 je	438 jf	439 jg	440 jh	441 ji	442 jj	443 jk	444 jl	445 jm	446 jn	447 jo	448 jp	449 jq	450 jr	451 js	452 jt	453 ju	454 jv	455 jw	456 jx	457 jy	458 jz	459 ka	460 kb	461 kc	462 kd	463 ke	464 kf	465 kg	466 kh	467 ki	468 kj	469 kk	470 kl	471 km	472 kn	473 ko	474 kp	475 kq	476 kr	477 ks	478 kt	479 ku	480 kv	481 kw	482 kx	483 ky	484 kz	485 la	486 lb	487 lc	488 ld	489 le	490 lf	491 lg	492 lh	493 li	494 lj	495 lk	496 ll	497 lm	498 ln	499 lo	500 lp	501 lq	502 lr	503 ls	504 lt	505 lu	506 lv	507 lw	508 lx	509 ly	510 lz	511 ma	512 mb	513 mc	514 md	515 me	516 mf	517 mg	518 mh	519 mi	520 mj	521 mk	522 ml	523 mn	524 mo	525 mp	526 mq	527 mr	528 ms	529 mt	530 mu	531 mv	532 mw	533 mx	534 my	535 mz	536 na	537 nb	538 nc	539 nd	540 ne	541 nf	542 ng	543 nh	544 ni	545 nj	546 nk	547 nl	548 nm	549 no	550 np	551 nq	552 nr	553 ns	554 nt	555 nu	556 nv	557 nw	558 nx	559 ny	560 nz	561 oa	562 ob	563 oc	564 od	565 oe	566 of	567 og	568 oh	569 oi	570 oj	571 ok	572 ol	573 om	574 on	575 oo	576 op	577 oq	578 or	579 os	580 ot	581 ou	582 ov	583 ow	584 ox	585 oy	586 oz	587 pa	588 pb	589 pc	590 pd	591 pe	592 pf	593 pg	594 ph	595 pi	596 pj	597 pk	598 pl	599 pm	600 pn	601 po	602 pp	603 pq	604 pr	605 ps	606 pt	607 pu	608 pv	609 pw	610 px	611 py	612 pz	613 qa	614 qb	615 qc	616 qd	617 qe	618 qf	619 qg	620 qh	621 qi	622 qj	623 qk
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[illegible]

[illegible]

Tel.: (301) 496-1350
 Email: robert.steuhrke@nih.gov
 Pinar: robert.steuhrke@nih.gov
 CNM Library Print: ATCC
 CNM Library Archived: ATCC
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing by: National Institutes of Health Intramural
 Clone distributor: (NISC) clone distribution information can be
 found through the K.M.G.E. database
 www.bio.lni.gov/bioby/image/image.html
 p:bio.lni.gov/bioby/image/image.html
 Seq primer: 2146-2157
 Location/Origin: 2119 (AB1).

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alignment_scores:
  Quality: 1058.00
  Ratio: 4.831
  Percent Similarity: 96.903
  Alignment Block:
    US-09-254-590-19 x AW413111
    ..
Align seq 1/1 (from: AW41311) to: 590

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[illegible]

Tue May 15 08:41:29 2001

us-09-254-590-19.fst

FEATURES

Source

REFERENCE

ATTHIONS

Journal

COMMENT

tel: (301) 496-1550

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308 GTCCAGAGCCATTATAGAGAGTGGAGTCTCTGTATATTACAAATTA 357
162 .....
338 AACCTTACCTCTGATMAACACCCCTGGCATCCACAAACACTAGCTG 407
163 .....
348 ..... Ala SerLeuTyrSerLeuA 169
408 TCCGAAATCCGTCTCTCATCTTCTCTAGAAATGCGATATATCCAG 457
169 TAAATGTCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 185
458 TCCGAAATCCGTCTCTCATCTTCTCTAGAAATGCGATATATCCAG 507
186 TAAATGTCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 192
508 GTATATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357
192 .....
558 GAAATCTATTATATATAGACACACACACCTCCCTGAAATGATCA 607
193 ..... Ile GlnLeuPheValAlaPheVal 202
608 GTGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 657
202 AAGAAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 219
658 AAGAAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 707
219 GCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
708 TGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 757
236 TCTCTPThAlaGlyAlaPheSerTyrAlaPheSerThrThAl 252
758 AACTGACACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 807
252 AAGPAlaPLeIleLeuSerIleProMetPheLeuAlaGlyTyrLeu 269
808 TGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 857
269 TAAATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
856 TGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 907
286 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
908 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
302 TAAATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319
958 GAAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1007
319 TGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
      ::::: |||
1008 TGAACCCCTG 1018

```


Genome version 4.5
Copyright (c) 1993 - 2000 Compaq Inc.

OK protein - protein search, using sw model

Run on: May 14, 2001, 18:47:21 : Search time 31.95 seconds

100.321 Million cell updates/sec

Title: US-09-254-590-19

Sequence: 1 NSSCPNCGWRRPSSLSNLS.....SSSRSSSSSAFPTSSSS 579

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 371700 seqs, 11207915 residues

Total number of hits satisfying chosen parameters: 374700

Maximum db seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: sp_arctaea.*
2: sp_bacteria.*
3: sp_eukarya.*
4: sp_fungi.*
5: sp_invertebrate.*
6: sp_mammals.*
7: sp_plants.*
8: sp_protozoa.*
9: sp_unclassified.*
10: sp_unclassified.*
11: sp_unclassified.*
12: sp_unclassified.*
13: sp_unclassified.*
14: sp_virus.*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2893.5	98.0	580 11 P70604	P70604. gallus galli
2	2135.5	72.0	736 4 O9016	O9016. homo sapien
3	2121.5	71.8	732 11 P70605	P70605. ratius nov
4	1868.5	63.3	561 4 O92952	O92952. homo sapien
5	1779.5	60.2	536 11 P70606	P70606. ratius nov
6	1684.5	50.7	5 02436	O2436. ratius nov
7	1684.5	50.7	5 02436	O2436. ratius nov
8	1684.5	50.7	5 02436	O2436. ratius nov
9	1684.5	50.7	5 02436	O2436. ratius nov
10	1684.5	50.7	5 02436	O2436. ratius nov
11	1684.5	50.7	5 02436	O2436. ratius nov
12	1684.5	50.7	5 02436	O2436. ratius nov
13	1684.5	50.7	5 02436	O2436. ratius nov
14	1684.5	50.7	5 02436	O2436. ratius nov
15	1684.5	50.7	5 02436	O2436. ratius nov
16	1684.5	50.7	5 02436	O2436. ratius nov
17	1684.5	50.7	5 02436	O2436. ratius nov
18	1684.5	50.7	5 02436	O2436. ratius nov
19	1684.5	50.7	5 02436	O2436. ratius nov
20	1684.5	50.7	5 02436	O2436. ratius nov

20	182	6.1	897 4 O9016	O9016. homo sapien
21	179	5.6	878 11 O9016	O9016. homo sapien
22	165.5	5.6	861 4 O9016	O9016. homo sapien
23	163	5.5	874 11 O9016	O9016. homo sapien
24	163	5.5	874 11 O9016	O9016. homo sapien
25	156.5	5.3	844 4 O9016	O9016. homo sapien
26	156.5	5.3	844 4 O9016	O9016. homo sapien
27	156.5	5.3	844 4 O9016	O9016. homo sapien
28	156.5	5.3	844 4 O9016	O9016. homo sapien
29	155.5	5.3	844 4 O9016	O9016. homo sapien
30	155.5	5.3	844 4 O9016	O9016. homo sapien
31	155.5	5.3	844 4 O9016	O9016. homo sapien
32	155.5	5.3	844 4 O9016	O9016. homo sapien
33	155.5	5.3	844 4 O9016	O9016. homo sapien
34	155.5	5.3	844 4 O9016	O9016. homo sapien
35	154.5	5.2	844 4 O9016	O9016. homo sapien
36	154.5	5.2	844 4 O9016	O9016. homo sapien
37	154.5	5.2	844 4 O9016	O9016. homo sapien
38	154.5	5.2	844 4 O9016	O9016. homo sapien
39	154.5	5.2	844 4 O9016	O9016. homo sapien
40	154.5	5.2	844 4 O9016	O9016. homo sapien
41	154.5	5.2	844 4 O9016	O9016. homo sapien
42	154.5	5.2	844 4 O9016	O9016. homo sapien
43	154.5	5.2	844 4 O9016	O9016. homo sapien
44	154.5	5.2	844 4 O9016	O9016. homo sapien
45	148.5	5.0	872 4 O9016	O9016. homo sapien

ALIGNMENTS

Result ID	Query Match	Score	DB ID	Description
1	98.0%	2893.5	580 11	P70604
2	72.0%	2135.5	736 4	O9016
3	71.8%	2121.5	732 11	P70605
4	63.3%	1868.5	561 4	O92952
5	60.2%	1779.5	536 11	P70606
6	50.7%	1684.5	5 02436	O2436
7	50.7%	1684.5	5 02436	O2436
8	50.7%	1684.5	5 02436	O2436
9	50.7%	1684.5	5 02436	O2436
10	50.7%	1684.5	5 02436	O2436
11	50.7%	1684.5	5 02436	O2436
12	50.7%	1684.5	5 02436	O2436
13	50.7%	1684.5	5 02436	O2436
14	50.7%	1684.5	5 02436	O2436
15	50.7%	1684.5	5 02436	O2436
16	50.7%	1684.5	5 02436	O2436
17	50.7%	1684.5	5 02436	O2436
18	50.7%	1684.5	5 02436	O2436
19	50.7%	1684.5	5 02436	O2436
20	50.7%	1684.5	5 02436	O2436

Tue May 15 08:41:28 2001

us-09-254-590-19.rsp

Page 4

[illegible][illegible][illegible][illegible]

Query Match	63.38	Score 1868.5	DB 4	Length 561
Best Local Similarity	70.38	Pred. No. 1.2e-124		
Matches 378: Conservative	46	Mismatches 70		

Query Match	60.28;	Score 1779.5;	DB 11;	Length 536
-------------	--------	---------------	--------	------------

Tue May 15 08:41:28 2001

us-09-254-590-19.rsp

Page 5

[illegible][illegible]

IR TSPRO, 178001222).
 KW Ionic channel.
 SO SEQUENCE 424 AA: 4759 MW: 808746CD07846AD CIRC44;
 Query Match 30.0%, Score 886.5; DB 11; Length 424;
 Meet Local Similarity 44.8% (Prod. No. 310655;
 Matches 189; Conservative 72; Mismatches 146; Indels 13; Gaps 4;
 0Y 121 LGHBALEPRKREGLSGALFQMGVATFTELSNVDKATSLKSLKSLSTT 180
 1b 121 LERRKRLLEDRGAKLVAGVIGTQITLADLRDQVATLVLVLTITVITAF 71
 0Y 181 LGLTYINRABSTAPROVAKQDNRIAMTREFECLTICVATIRP-CNTTTPQA 239
 1b 181 LGLTYINRABSTAPROVAKQDNRIAMTREFECLTICVATIRP-CNTTTPQA 239
 0Y 240 BLATVSTTTADDTITITITPRTATYLAIVMLKSLFPTDSQSLAKNTINTR 295
 1b 72 LGLTYINRABSTAPROVAKQDNRIAMTREFECLTICVATIRP-CNTTTPQA 239
 0Y 300 FAKTQWMTFGLRERELSLAKLDELTPVAVLSSQVFLANSTVSTGLANQVFRM 359
 1b 132 FAKTQWMTFGLRERELSLAKLDELTPVAVLSSQVFLANSTVSTGLANQVFRM 359
 0Y 192 FAKLMTNIRLRLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 449
 1b 192 FAKLMTNIRLRLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 449
 0Y 360 GVGQVPTQCGKGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 419
 1b 360 GVGQVPTQCGKGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 419
 0Y 420 KKAALNDELSTLTKTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTK 479
 1b 420 KKAALNDELSTLTKTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTK 479
 0Y 310 KESARLGLDAMTK 366
 1b 310 KESARLGLDAMTK 366
 0Y 460 VGLATQNTNIRNLSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSL 419
 1b 460 VGLATQNTNIRNLSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSL 419
 0Y 367 VDISMIRLCTDGLSIRSLRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIR 419
 1b 367 VDISMIRLCTDGLSIRSLRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIR 419
 0Y 540 IE 541
 1b 420 ID 421
 RESULT 14
 ID 015554 PRELIMINARY; PRT: 427 AA.
 DT 01-JAN-1998 (TDBLevel: 05, Created)
 DT 01-JUN-2000 (TDBLevel: 13, Last sequence update)
 DT 01-JUN-2000 (TDBLevel: 14, Last annotation update)
 DE IMMEDIATE CONDUCTANCE CHANNEL-ACTIVATED POTASSIUM
 DE IMMEDIATE CONDUCTANCE CHANNEL-ACTIVATED POTASSIUM
 DE GARDOS CHANNEL
 CH HCKC OR HS24 OR 1X1.
 CC CC
 CC Bacteria: Streptococcus; Chlamidia; Vertebrata; Eukaryotes; Mammalia; Balaenidae; Primates; Cetartia; Invertebrata; Homo.
 CC NCBI: TaxID=9606.
 RP SEQUENCE FROM N.A.
 RA Genshiani S., Genshiani M., Bu A.C.-L., Gargus J.J., Genshiani G.A.,
 RL Submitted (Nov-1997) to the EMBL/Genbank/DBJ databases.
 NM 12
 RS SEQUENCE FROM N.A.
 RC MEDLINE=97454570;
 RA Jolier M.J., Wang L.Y., Tang M.D., Kuczmarsk L.K.;
 RM (13) Medl. Acad. Sci. U.S.A. 96:11015-11018(1997).
 RP SEQUENCE FROM N.A.
 RA Jolier M.J., Wang L.Y., Tang M.D., Kuczmarsk L.K.;
 RM (13) Medl. Acad. Sci. U.S.A. 96:11015-11018(1997).
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.

RP SEQUENCE FROM N.A.
 RC TISSUE=LYNTH NODE;
 RA Houston M.O., Wang J., Tong J.A.,
 PT A novel gene, hckcd, encodes the calcium-activated potassium channel
 IN h human lymphocytes; 33726(1997).
 NM 151
 RP SEQUENCE FROM N.A.
 RA Maylie J., Slyvia C., Hirschberg B., Bond C.T., Mewman J.P.,
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
 RP SEQUENCE OR 227-367 FROM N.A.
 RA Golding S., Culliford S.J., Eliory J.C.;
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 RBH: AF033621, AAC3604.1;
 RBH: AF032297, AAC3133.1;
 RBH: AF032150, AAC3341.1;
 RBH: AF032040, AAC3261.1;
 RM (13) Medl. Acad. Sci. U.S.A. 96:11015-11018(1997).
 KW Ionic channel.
 SO SEQUENCE 427 AA: 4759 MW: 23F9FA66094410F CIRC54;
 Query Match 29.0%, Score 880.5; DB 4; Length 427;
 Meet Local Similarity 44.8% (Prod. No. 310655;
 Matches 189; Conservative 71; Mismatches 131; Indels 43; Gaps 7;
 0Y 121 LGHBALEPRKREGLSGALFQMGVATFTELSNVDKATSLKSLKSLSTT 180
 1b 121 LERRKRLLEDRGAKLVAGVIGTQITLADLRDQVATLVLVLTITVITAF 71
 0Y 181 LGLTYINRABSTAPROVAKQDNRIAMTREFECLTICVATIRP-CNTTTPQA 239
 1b 181 LGLTYINRABSTAPROVAKQDNRIAMTREFECLTICVATIRP-CNTTTPQA 239
 0Y 240 BLATVSTTTADDTITITITPRTATYLAIVMLKSLFPTDSQSLAKNTINTR 295
 1b 72 LGLTYINRABSTAPROVAKQDNRIAMTREFECLTICVATIRP-CNTTTPQA 239
 0Y 300 FAKTQWMTFGLRERELSLAKLDELTPVAVLSSQVFLANSTVSTGLANQVFRM 359
 1b 132 FAKTQWMTFGLRERELSLAKLDELTPVAVLSSQVFLANSTVSTGLANQVFRM 359
 0Y 192 FAKLMTNIRLRLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 449
 1b 192 FAKLMTNIRLRLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 449
 0Y 360 GVGQVPTQCGKGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 419
 1b 360 GVGQVPTQCGKGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 419
 0Y 420 KKAALNDELSTLTKTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTK 479
 1b 420 KKAALNDELSTLTKTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTKLTK 479
 0Y 310 KESARLGLDAMTK 366
 1b 310 KESARLGLDAMTK 366
 0Y 460 VGLATQNTNIRNLSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSL 419
 1b 460 VGLATQNTNIRNLSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSLNSL 419
 0Y 367 VDISMIRLCTDGLSIRSLRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIR 419
 1b 367 VDISMIRLCTDGLSIRSLRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIRIR 419
 0Y 540 IE 541
 1b 420 ID 421
 RESULT 15
 ID 015554 PRELIMINARY; PRT: 196 AA.
 DT 01-JAN-1998 (TDBLevel: 13, Created)
 DT 01-JUN-2000 (TDBLevel: 13, Last sequence update)
 DT 01-JUN-2000 (TDBLevel: 13, Last annotation update)
 DE IMMEDIATE CONDUCTANCE CHANNEL-ACTIVATED POTASSIUM
 DE IMMEDIATE CONDUCTANCE CHANNEL-ACTIVATED POTASSIUM
 DE GARDOS CHANNEL
 CH HCKC OR HS24 OR 1X1.
 CC CC
 CC Bacteria: Streptococcus; Chlamidia; Vertebrata; Eukaryotes; Mammalia; Balaenidae; Primates; Cetartia; Invertebrata; Homo.
 CC NCBI: TaxID=9606.
 RP SEQUENCE FROM N.A.
 RA Genshiani S., Genshiani M., Bu A.C.-L., Gargus J.J., Genshiani G.A.,
 RL Submitted (Nov-1997) to the EMBL/Genbank/DBJ databases.
 NM 12
 RS SEQUENCE FROM N.A.
 RC MEDLINE=97454570;
 RA Jolier M.J., Wang L.Y., Tang M.D., Kuczmarsk L.K.;
 RM (13) Medl. Acad. Sci. U.S.A. 96:11015-11018(1997).
 RP SEQUENCE FROM N.A.
 RA Jolier M.J., Wang L.Y., Tang M.D., Kuczmarsk L.K.;
 RM (13) Medl. Acad. Sci. U.S.A. 96:11015-11018(1997).
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.

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OK protein - protein search, using sw model

Run on: May 14, 2001, 18:48:35 : Search time 11.16 seconds

Seq on: 1158000000 : 636,519 million cell updates/sec

File: us-09-254-590-19

Perfect score: 2554

Sequence: 1 MSRCRNGWPRSLNS.....SSSRHSSTAFSSSS 579

Scoring table:

Gapop 10.0 / Repeat 0.5

Searched: 93435 seep, 34255466 residues

Total number of hits satisfying chosen parameters: 93435

Minimum hit seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: swsaproct.39+

Result No. 18 the number of results predicted by chance to have a

score of 18 or more than the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	669	22.6	471	YX1L.CARL	01122 casorabid1
2	160	6.4	825	C10L.JUMAN	04355 homo sapien
3	160	6.4	825	C10L.JUMAN	04355 homo sapien
4	166	5.6	924	C1R6.DROME	01303 homo sapien
5	148	5.1	797	C1R6.JUMAN	01303 homo sapien
6	148	5.1	797	C1R6.JUMAN	01303 homo sapien
7	144	4.9	889	C1R7.BAT	001956 ratia nov
8	141	5.5	824	C1A5.BEAT	R6144 cytochrome
9	141	5.5	824	C1A5.BEAT	R6144 cytochrome
10	138	4.7	436	EXX2.JUMAN	000828 homo sapien
11	137	4.7	436	EXX2.JUMAN	000828 homo sapien
12	134	4.6	540	C1R6.DROME	004609 ratia nov
13	134	4.6	540	C1R6.DROME	004609 ratia nov
14	134	4.6	540	C1R6.DROME	004609 ratia nov
15	134	4.6	540	C1R6.DROME	004609 ratia nov
16	134	4.6	540	C1R6.DROME	004609 ratia nov
17	133	4.5	391	BH6L.JUMAN	009525 homo sapien
18	132	4.5	635	C1R6.BAT	063734 ratia nov
19	132	4.5	635	C1R6.BAT	063734 ratia nov
20	129	4.2	604	C10L.JUMAN	P9744 mus musculu
21	128	4.4	671	BH6C.DROME	P23810 dicophylla
22	128	4.4	671	BH6C.DROME	P23810 dicophylla
23	125	4.2	440	C10L.JUMAN	P1387 ratia nov
24	125	4.2	440	C10L.JUMAN	P1387 ratia nov
25	125	4.2	440	C10L.JUMAN	P1387 ratia nov
26	125	4.2	440	C10L.JUMAN	P1387 ratia nov
27	123	4.1	497	BH6L.JUMAN	P23810 dicophylla
28	121	4.1	638	C1R6.BAT	063734 ratia nov
29	120	4.1	638	C1R6.BAT	063734 ratia nov
30	120	4.1	638	C1R6.BAT	063734 ratia nov
31	120	4.1	638	C1R6.BAT	063734 ratia nov
32	119	4.0	500	BH6L.JUMAN	P23810 dicophylla
33	118	4.0	500	BH6L.JUMAN	P23810 dicophylla

34	118	4.0	167	1 SGE.DROME	P18431 dicophylla
35	117	4.0	367	1 R613.KSNU	009029 mesocricetu
36	117	4.0	508	1 C1R6.DROME	P32027 dicophylla
37	116	3.9	140	1 C1A4.DROME	003100 dicophylla
38	116	3.9	140	1 C1A4.DROME	003100 dicophylla
39	116	3.9	369	1 MV2.BAT	P4844 ratia nov
40	116	3.9	679	1 R613.KSNU	P23810 dicophylla
41	116	3.9	679	1 R613.KSNU	P23810 dicophylla
42	115	3.9	919	1 BHR6.JUMAN	P10275 homo sapien
43	115	3.9	165	1 GRP1.DROME	P25074 oryza sativ
44	115	3.9	165	1 GRP1.DROME	P25074 oryza sativ
45	115	3.9	410	1 BHR6.JUMAN	012837 homo sapien

ALIGNMENTS

Result No.	Score	Query	Length	DB ID	Description
1	669	22.6	471	YX1L.CARL	01122 casorabid1
2	160	6.4	825	C10L.JUMAN	04355 homo sapien
3	160	6.4	825	C10L.JUMAN	04355 homo sapien
4	166	5.6	924	C1R6.DROME	01303 homo sapien
5	148	5.1	797	C1R6.JUMAN	01303 homo sapien
6	148	5.1	797	C1R6.JUMAN	01303 homo sapien
7	144	4.9	889	C1R7.BAT	001956 ratia nov
8	141	5.5	824	C1A5.BEAT	R6144 cytochrome
9	141	5.5	824	C1A5.BEAT	R6144 cytochrome
10	138	4.7	436	EXX2.JUMAN	000828 homo sapien
11	137	4.7	436	EXX2.JUMAN	000828 homo sapien
12	134	4.6	540	C1R6.DROME	004609 ratia nov
13	134	4.6	540	C1R6.DROME	004609 ratia nov
14	134	4.6	540	C1R6.DROME	004609 ratia nov
15	134	4.6	540	C1R6.DROME	004609 ratia nov
16	134	4.6	540	C1R6.DROME	004609 ratia nov
17	133	4.5	391	BH6L.JUMAN	009525 homo sapien
18	132	4.5	635	C1R6.BAT	063734 ratia nov
19	132	4.5	635	C1R6.BAT	063734 ratia nov
20	129	4.2	604	C10L.JUMAN	P9744 mus musculu
21	128	4.4	671	BH6C.DROME	P23810 dicophylla
22	128	4.4	671	BH6C.DROME	P23810 dicophylla
23	125	4.2	440	C10L.JUMAN	P1387 ratia nov
24	125	4.2	440	C10L.JUMAN	P1387 ratia nov
25	125	4.2	440	C10L.JUMAN	P1387 ratia nov
26	125	4.2	440	C10L.JUMAN	P1387 ratia nov
27	123	4.1	497	BH6L.JUMAN	P23810 dicophylla
28	121	4.1	638	C1R6.BAT	063734 ratia nov
29	120	4.1	638	C1R6.BAT	063734 ratia nov
30	120	4.1	638	C1R6.BAT	063734 ratia nov
31	120	4.1	638	C1R6.BAT	063734 ratia nov
32	119	4.0	500	BH6L.JUMAN	P23810 dicophylla
33	118	4.0	500	BH6L.JUMAN	P23810 dicophylla

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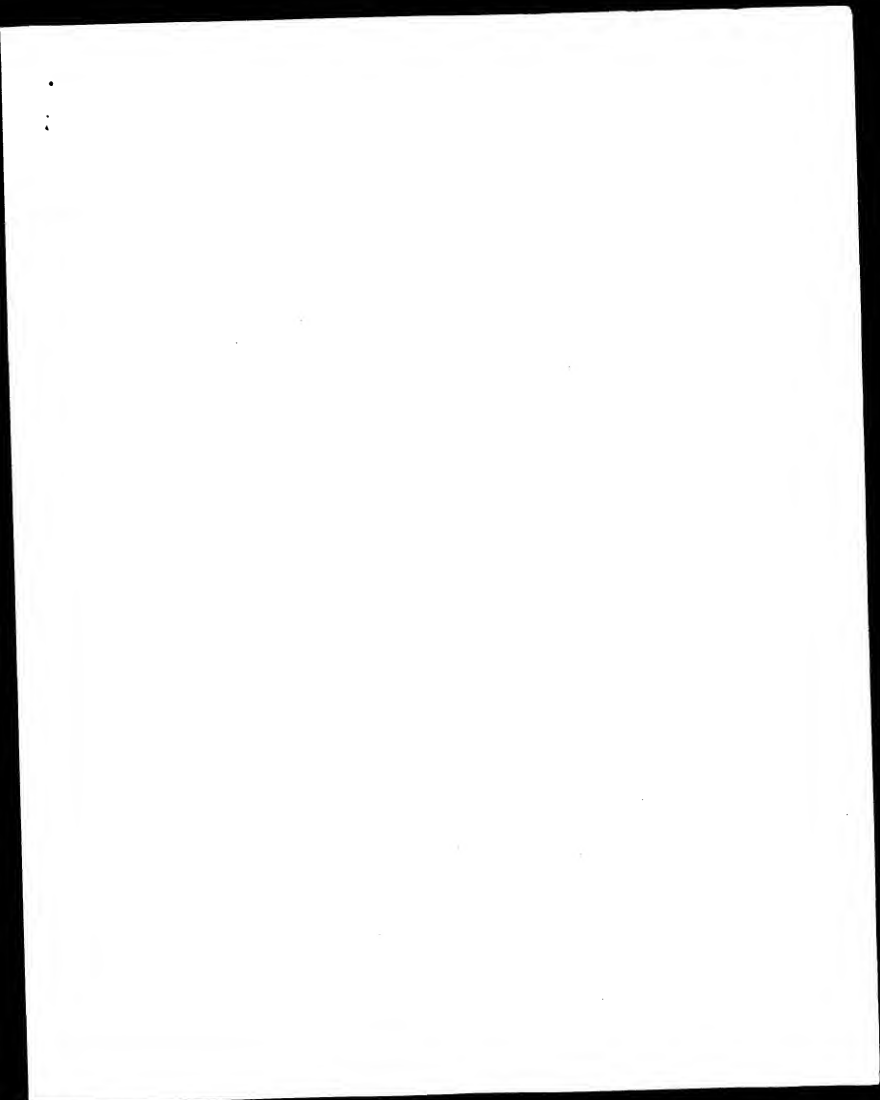
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Db 387 TWIYAEIKNRSDPRNDITPRNIPISGPMWY-VTWTTLEIYSNPRFMSDNRDNL 435
Oy 375 CLTCEIMKNCALY-----AVASRELEIFKAERW 406
Db 456 CALAGVITLMPPTIVNRENYSANAKCLP-KRKKRY 496

Search completed: May 14, 2001, 20:41:38
Job time: 8803 sec



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OM protein - protein search, using sw model

Run on: May 14, 2001, 17:53:00 : Search Name 42.31 Google

Title: 05-09-234-590-19

Perfect score: 2554

Sequence: 1 MSRRKNGWVGRSLNSLS.....SSSRKRSSTAVFTSSSS 379

Scoring table:

Gap 10.0 , Gapext 0.5

Searched: 198801 seqs, 6872935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum db seq length: 0

Maximum db seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database:

1: p11.1

2: p11.2

3: p11.3

4: p11.4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	DB	ID	Description
1	2118.5	71.7	702	2	T24351	hypothetical protein
2	1902.5	69.5	702	2	T24351	hypothetical protein
3	902	30.5	925	2	T18747	hypothetical protein
4	669	22.6	411	2	T15354	hypothetical protein
5	669	22.6	411	2	T15354	hypothetical protein
6	156.5	5.3	353	2	J55275	volcanic-sulfate
7	151.5	5.2	924	2	B11359	potassium channel
8	151.5	5.2	924	2	B11359	potassium channel
9	150.5	5.1	924	2	B12746	potassium channel
10	147	5.0	489	2	J54287	shw protein - Cat
11	146.5	4.9	639	2	T00526	volcanic-sulfate
12	146.5	4.9	639	2	T00526	volcanic-sulfate
13	144	4.9	484	2	T24238	hypothetical protein
14	142	4.8	484	2	T24238	hypothetical protein
15	142	4.8	484	2	T24238	hypothetical protein
16	142	4.8	484	2	T24238	hypothetical protein
17	138.5	4.7	333	2	A39065	homoeotic protein B
18	138.5	4.7	333	2	A39065	homoeotic protein B
19	131.7	4.6	776	2	T20896	hypothetical protein
20	136.5	4.6	1728	2	T14603	hypothetical protein
21	135	4.6	480	2	A35312	potassium channel
22	134.5	4.6	645	2	T27186	hypothetical protein
23	134.5	4.6	645	2	T27186	hypothetical protein
24	134.5	4.6	645	2	T27186	hypothetical protein
25	133.5	4.5	645	2	T27186	hypothetical protein
26	133.5	4.5	645	2	T27186	hypothetical protein
27	132	4.5	692	2	S13138	potassium channel
28	132	4.5	692	2	S13138	potassium channel
29	131	4.4	1037	2	T31554	probable potassium

30	130	4.4	688	2	S53349	potassium channel
31	128.5	4.4	236	2	I53681	potassium channel
32	128.5	4.4	671	2	A35932	homoeotic protein B
33	128.5	4.4	671	2	A35932	homoeotic protein B
34	128.5	4.4	671	2	A35932	homoeotic protein B
35	125.5	4.2	591	2	S17150	transcription factor
36	125.5	4.2	453	1	C60701	potassium channel
37	125.5	4.2	453	1	C60701	potassium channel
38	125	4.2	549	2	B33372	male-specific double
39	123.5	4.2	857	2	I55529	potassium channel
40	123.5	4.2	857	2	I55529	potassium channel
41	122.5	4.1	1384	2	T11168	potassium channel
42	121.5	4.1	596	2	A41395	adenylyl cyclase cy
43	121.5	4.1	624	2	S27203	volcanic-sulfate
44	121.5	4.1	1184	2	A43504	adenylyl cyclase cy
45	121.5	4.1	1184	2	A43504	adenylyl cyclase cy

ALIGNMENTS

RESULT 1

Probable calcium-activated potassium channel KCNQ3 - human

Accession: T09172

Release: 20-Sep-1999 sequence revision: 20-Sep-1999 #ext: change 11-May-2000

Author: 1999, E. J. Wittekindt, O. J. Adams, K. J. Song, L. L. Ho, T. H. Gatten

NO: Psycholgy 3, 32-37, 1998

Ar:Title: Isolation of a novel potassium channel gene hSKC3 containing a polymorphic

Ar:Accession: U09312

Ar:Accession: U09312

Ar:Status: translated from cDNA/EMBL/DBU

Ar:Molecule type: RNA

Ar:Accession: U09312

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Ar:Accession: U09312

Ar:Accession: U09312

Tue May 15 08:41:26 2001

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Oy 139 LIFONGCIYVWIFTEISNGADASYSIAKCLISLSTILLIGLIYVHARELOFWV 198
Oy 203 -----GNV-----LISGN-----OCALM-----LOIFRS 221
Oy 199 DNGADOMKIANTYERHIF-----ICLILYVIAHPICONTITVIAEASYSAS 248
Oy 222 KRFSD KIERTOYVIFRMOSSELWIAVIVOLY-----MADRASAP 267
Oy 249 TTAOVOLISIPERFLACLIANWUJISKLTJASNSICOLAKINRTRWKTLMTI 308
Oy 268 P-----LOIPYIAVIAVOTLWVACNBA-----FRODHGIA 304
Oy 309 CROTLVNSISSEHIANVUNACENWDOOVSNGAMELISITTSICGOMRPT 368
Oy 305 CYALIAVYAVVOLLPOPSNSE-----GIMV-TVFYITTY-TLP-- 347
Oy 369 YOCBOVCLITGIMOGCTLYAVVARKLEFYAKEXHVRNPMQOLTERYMAAYVR 428
Oy 348 -VNRBAVYSOVL--LSTHIALALF--TNAO--DRETL-----KOLVSNV-- 386
Oy 429 ETNLIYVFKIKEDIAVRIQOFLOIHOUISVYKROKNDKNDANTLOVLATONI 488
Oy 387 ---LISCEINVOCHERFANOSMONDETRELOANUSKREKODERLLSVZPRHV 443
Oy 489 MTOMI SOLJESSED--FERKHYTLLETLISIHAKOLISQTHOQOQRPIDQMS 546
Oy 444 ANEKAKIYAKODMWRKTYIOKHDFEILNADIEPTSLASCAQOLWVMEFLAS 503
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Oy 504 FPKIAEN 511

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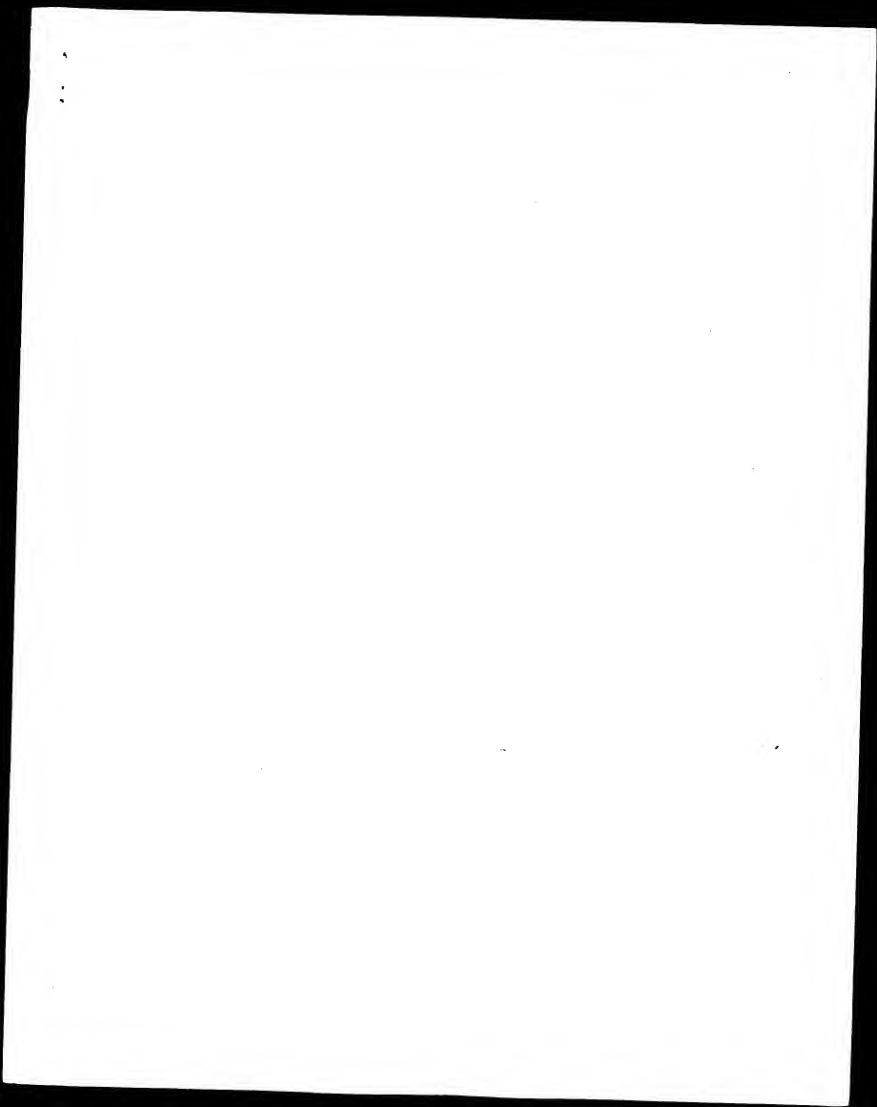
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Page 22

Tue May 15 08:41:35 2001

us-09-254-590-21.rst

Page 13



Align seg 1/1 to: V35457 from: 1 to: 1740

[illegible]

[illegible]


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138 GATCTCTCCAGGAGAGATACAGATCCGACAGATCTCTCTCATACGC
84 hcdlycy ..... ghyhscfthghyghy 94
188 CCAAGCTCTCCACACACACACACACACACACACACACACACACAC
95 ghyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
229 ..... GCGACACACACACACACACACACACACACACACACAC
111 altyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
128 ..... GCGACACACACACACACACACACACACACACACACAC
238 GCGACACACACACACACACACACACACACACACACACACACACAC
307 hcdlyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
128 hcdlyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
308 hcdlyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
145 ghylghyghyghyghyghyghyghyghyghyghyghyghyghyghy
358 GCGACACACACACACACACACACACACACACACACACACACACAC
161 ghylghyghyghyghyghyghyghyghyghyghyghyghyghyghy
408 AAGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
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194 ..... GCGACACACACACACACACACACACACACACACACAC
458 CCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
407 hcdlyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
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228 ..... GCGACACACACACACACACACACACACACACACACAC
608 CCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
558 hcdlyghyghyghyghyghyghyghyghyghyghyghyghyghyghy
228 ghylghyghyghyghyghyghyghyghyghyghyghyghyghyghy
446 ..... GCGACACACACACACACACACACACACACACACACAC
608 CCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
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245 ghylghyghyghyghyghyghyghyghyghyghyghyghyghyghy
261 ..... GCGACACACACACACACACACACACACACACACACAC
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708 ghylghyghyghyghyghyghyghyghyghyghyghyghyghyghy
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957 ..... GCGACACACACACACACACACACACACACACACACAC
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361 ..... GCGACACACACACACACACACACACACACACACACAC
958 ghylghyghyghyghyghyghyghyghyghyghyghyghyghyghy
1007 ..... GCGACACACACACACACACACACACACACACACACAC
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378 ..... GCGACACACACACACACACACACACACACACACACAC
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1108 GCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1157 ..... GCGACACACACACACACACACACACACACACACACAC
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XX W0931139.AL.

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Tue May 15 08:41:21 2001

us-09-254-590-19.rng

Page 22

[illegible]

US-09-254-590-19.rai

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: Picturix 0.05/MS-DOS
APPLICATION: Picturix Runes #1.0, Version #1.25
FLYING DATE: 06-JUN-1994
PRECISION: 100%
APPLICATION:
APPLICATION NUMBER: 18
ATTN DATE: 11-FEB-1994
NAME: Bonnet, INFORMATION:
REGISTRATION NUMBER: 34,547
TELECOMMUNICATIONS NUMBER: C-270/3
TELEPHONE: (313)37-6966
INFORMATION FOR #13137-6972
SEQUENCE CHARACTERISTICS: 148
TYPE: 317 amino acids
STRANDS: 1
STRANDS: 1
MOLCULAR WEIGHT: linear
MW: 14846.468-6094.148 Protein

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 SEQUENCE 1165 148
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 TITLE OF INVENTION: MULTIVARIANT II-3 HEMAGGLUTININ
 NUMBER OF SEQUENCES: 136
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 COMPUTER: IBM PC COMPATIBLE
 SOFTWARE: SYSTIM: PC-DOS/MS-DOS
 CURRENT APPLICATION NUMBER: 1.0, Version #1.30 (PRO)
 FILING DATE: 02 FEB 1995
 CLASSIFICATION: PC/TG9501185
 PAPER APPLICATION DATA:
 PAPER NUMBER: US 08/192325
 FILING DATE:

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Query Match      4.13;      Score 120.5; DB 5; length 337
Best Local Similarity 34.68; Pred. No. 0.01;

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Sequence 49, Application US/08475411A
Patent No. 6140072
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.

file May 15 08:41:18 2001

us -09-254-590-19 .ral

APPLICANT: Capello, Joseph
 TITLE OF INVENTION: Synthetic Protein Polymer
 NUMBER OF SEQUENCES: 119
 CORRESPONDENCE: Fleher, Hoback, Teal, Attribution & Heartbe
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/478,023A
 FILING DATE: 07-20-1995
 CLASSIFICATION DATA:
 PREVIOUS APPLICATION NUMBER: US 07/609,716
 FILING DATE: 06-01-1990
 APPLICATION NUMBER: US 07/269,429
 FILING DATE: 09-04-1988
 PRIOR APPLICATION NUMBER: US 07/114,618
 FILING DATE: 09-04-1987
 PRIOR APPLICATION NUMBER: US 06/927,258
 FILING DATE: 10-03-1983
 FILING DATE: 04-NOV-1986
 REGISTRATION NUMBER: A-55186-9/RT/MTK
 REPRESENTATION INFORMATION:
 NAME: TRECOTIL, Richard F.
 TELEPHONE: 415-761-1989
 TELEFAX: 415-761-1989
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
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 STANDARDS: single
 TOPOLOG: linear
 MOLECULE TYPE: protein
 US-08-475-411A-49
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 Best Local Similarity 4.0%, Pred. No. 0.032, Indels 1; Gaps 1;
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 US-08-478-023A-49
 Application US/08/478023A
 Patent No. 6134348
 APPLICANT: Capello, Joseph A.
 TITLE OF INVENTION: Synthetic Protein Polymer
 NUMBER OF SEQUENCES: 119
 CORRESPONDENCE ADDRESS:

ADDRESS: Fleher, Hoback, Teal, Attribution & Heartbe
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2" floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/478,023A
 FILING DATE: 07-20-1995
 CLASSIFICATION DATA:
 PREVIOUS APPLICATION NUMBER: US 07/609,716
 FILING DATE: 06-01-1990
 APPLICATION NUMBER: US 07/269,429
 FILING DATE: 09-04-1988
 PRIOR APPLICATION NUMBER: US 07/114,618
 FILING DATE: 09-04-1987
 PRIOR APPLICATION NUMBER: US 06/927,258
 FILING DATE: 10-03-1983
 FILING DATE: 04-NOV-1986
 REGISTRATION NUMBER: A-55186-9/RT/MTK
 REPRESENTATION INFORMATION:
 NAME: TRECOTIL, Richard F.
 TELEPHONE: 415-761-1989
 TELEFAX: 415-761-1989
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 649 amino acids
 STANDARDS: single
 TOPOLOG: linear
 MOLECULE TYPE: protein
 US-08-478-023A-49
 Query Match 4.0%, Score 119.5, ID 4, Length 649;
 Best Local Similarity 4.0%, Pred. No. 0.032, Indels 1; Gaps 1;
 Matches 281 Conserved 8; Mismatches 33; Indels 1; Gaps 1;
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 US-08-478-023A-49
 Application US/08/478023A
 Patent No. 6027515
 APPLICANT: Capello, Joseph A.
 TITLE OF INVENTION: Multi-Topology Protein
 NUMBER OF SEQUENCES: 196
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2" floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION NUMBER: US/08/469,318

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Page 6

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2. General Information:
3. Application: Mine, William D.
4. Title of Invention: Soluble Peptide Having Constrained
5. Title of Invention: Same.
6. Number of Sequences: 174
7. Country: USA
8. Address: Campbell & Pierce LLP
9. Street: 4370 La Jolla Village Drive, Suite 700
10. State: California
11. Country: USA
12. Computer Hardware Form:
13. Medium Type: Floppy disk
14. Operating System: IBM PC compatible DOS
15. Software: Pileupin Release 41.0, Version 11.25
16. Computer Application Data: 03/09/440-787A
17. Filing Date: 15-MAY-1999
18. Classification: 435
19. Application Number: US 07/78,893
20. Filing Date: 10-NOV-1992
21. Name: Campbell, William D.
22. Registration Number: 31,815
23. Telephone: (619) 535-9001
24. Telex: 6139 535-9049
25. International Patent No.:
26. Sequence Characteristics: 51
27. Length: 7294 base pairs
28. Strandness: Double
29. Topology: Circular

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Patent No.: 5684426
GENERAL INFORMATION:
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
CORRESPONDENCE ADDRESS:
ADDRESSER: PERRY, SCHROEDER, BRIDGESMAN & CLARK
STREET: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: UNITED STATES
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release 11.0, Version 11.25
CURRENT ACTION NUMBER: US/08/464,136
FILING DATE:
CLASSIFICATION INFORMATION:
NAME: CAMPBELL, CATHERY A.
REGISTRATION NUMBER: 31,851,882
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 7317 base pairs
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US-08-464-136-2
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Percent similarity: 46.224 Percent identity: 24.256
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Page 11

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